



IFWO

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/823,506

DATE: 09/17/2004

TIME: 11:38:31

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Output Set: N:\CRF4\09172004\J823506.raw

1 <110> APPLICANT: Hellerqvist, Carl  
 2 Fu, Changlin  
 3 <120> TITLE OF INVENTION: GBS Toxin Receptor  
 4 <130> FILE REFERENCE: CARB-008/01US  
 5 <140> CURRENT APPLICATION NUMBER: US/10/823,506  
 6 <141> CURRENT FILING DATE: 2004-04-12  
 7 <150> PRIOR APPLICATION NUMBER: US/09/359,167  
 8 <151> PRIOR FILING DATE: 1999-07-21  
 9 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60-693,843  
 W--> 10 <151> PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-22  
 11 <160> NUMBER OF SEQ ID NOS: 12  
 12 <170> SOFTWARE: PatentIn Ver. 2.0  
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 15 <211> LENGTH: 2602  
 16 <212> TYPE: DNA  
 17 <213> ORGANISM: Homo sapiens  
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 19 <221> NAME/KEY: CDS  
 20 <222> LOCATION: (58)..(1542)  
 21 <400> SEQUENCE: 1

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24	Met Arg Ser Pro Val Arg Asp Leu Ala Arg Asn Asp Gly Glu Glu Ser	
25	1 5 10 15	
26	acg gac cgc acg cct ctt cta ccg ggc gcc cca cgg gcc gaa gcc gct	153
27	Thr Asp Arg Thr Pro Leu Leu Pro Gly Ala Pro Arg Ala Glu Ala Ala	
28	20 25 30	
29	cca gtg tgc tgc tct gct cgt tac aac tta gca att ttg gcc ttt ttt	201
30	Pro Val Cys Cys Ser Ala Arg Tyr Asn Leu Ala Ile Leu Ala Phe Phe	
31	35 40 45	
32	ggt ttc ttc att gtg tat gca tta cgt gtg aat ctg agt gtt gcg tta	249
33	Gly Phe Phe Ile Val Tyr Ala Leu Arg Val Asn Leu Ser Val Ala Leu	
34	50 55 60	
35	gtg gat atg gta gat tca aat aca act tta gaa gat aat aga act tcc	297
36	Val Asp Met Val Asp Ser Asn Thr Thr Leu Glu Asp Asn Arg Thr Ser	
37	65 70 75 80	
38	aag gcg tgt cca gag cat tct gct ccc ata aaa gtt cat cat aat caa	345
39	Lys Ala Cys Pro Glu His Ser Ala Pro Ile Lys Val His His Asn Gln	
40	85 90 95	
41	acg ggt aag aag tac caa tgg gat gca gaa act caa gga tgg att ctc	393
42	Thr Gly Lys Lys Tyr Gln Trp Asp Ala Glu Thr Gln Gly Trp Ile Leu	
43	100 105 110	
44	ggt tcc ttt ttt tat ggc tac atc atc aca cag att cct gga gga tat	441

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47	gtt gcc agc aaa ata ggg ggg aaa atg ctg cta gga ttt ggg atc ctt	489
48	Val Ala Ser Lys Ile Gly Gly Lys Met Leu Leu Phe Gly Ile Leu	
49	130 135 140	
50	ggc act gct gtc ctc acc ctg ttc act ccc att gct gca gat tta gga	537
51	Gly Thr Ala Val Leu Thr Leu Phe Thr Pro Ile Ala Ala Asp Leu Gly	
52	145 150 155 160	
53	gtt gga cca ctc att gta ctc aga gca cta gaa gga cta gga gag ggt	585
54	Val Gly Pro Leu Ile Val Leu Arg Ala Leu Glu Gly Leu Gly Glu Gly	
55	165 170 175	
56	gtt aca ttt cca gcc atg cat gcc atg tgg tct tct tgg gct ccc cct	633
57	Val Thr Phe Pro Ala Met His Ala Met Trp Ser Ser Trp Ala Pro Pro	
58	180 185 190	
59	ctt gaa aga agc aaa ctt ctt agc att tcg tat gca gga gca cag ctt	681
60	Leu Glu Arg Ser Lys Leu Leu Ser Ile Ser Tyr Ala Gly Ala Gln Leu	
61	195 200 205	
62	ggg aca gta att tct ctt cct ctt tct gga ata att tgc tac tat atg	729
63	Gly Thr Val Ile Ser Leu Pro Leu Ser Gly Ile Ile Cys Tyr Tyr Met	
64	210 215 220	
65	aat tgg act tat gtc ttc tac ttt ttt ggt act att gga ata ttt tgg	777
66	Asn Trp Thr Tyr Val Phe Tyr Phe Phe Gly Thr Ile Gly Ile Phe Trp	
67	225 230 235 240	
68	ttt ctt ttg tgg atc tgg tta gtt agt gac aca cca caa aaa cac aag	825
69	Phe Leu Leu Trp Ile Trp Leu Val Ser Asp Thr Pro Gln Lys His Lys	
70	245 250 255	
71	aga att tcc cat tat gaa aag gaa tac att ctt tca tca tta aga aat	873
72	Arg Ile Ser His Tyr Glu Lys Glu Tyr Ile Leu Ser Ser Leu Arg Asn	
73	260 265 270	
74	cag ctt tct tca cag aag tca gtg ccg tgg gta ccc att tta aaa tcc	921
75	Gln Leu Ser Ser Gln Lys Ser Val Pro Trp Val Pro Ile Leu Lys Ser	
76	275 280 285	
77	ctg cca ctt tgg gct atc gta gtt gca cac ttt tct tac aac tgg act	969
78	Leu Pro Leu Trp Ala Ile Val Val Ala His Phe Ser Tyr Asn Trp Thr	
79	290 295 300	
80	ttt tat act tta ttg aca tta ttg cct act tat atg aag gag atc cta	1017
81	Phe Tyr Thr Leu Leu Thr Leu Leu Pro Thr Tyr Met Lys Glu Ile Leu	
82	305 310 315 320	
83	agg ttc aat gtt caa gag aat ggg ttt tta tct tca ttg cct tat tta	1065
84	Arg Phe Asn Val Gln Glu Asn Gly Phe Leu Ser Ser Leu Pro Tyr Leu	
85	325 330 335	
86	ggc tct tgg tta tgt atg atc ctg tct ggt caa gct gct gac aat tta	1113
87	Gly Ser Trp Leu Cys Met Ile Leu Ser Gly Gln Ala Ala Asp Asn Leu	
88	340 345 350	
89	agg gca aaa tgg aat ttt tca act tta tgt gtt cgc aga att ttt agc	1161
90	Arg Ala Lys Trp Asn Phe Ser Thr Leu Cys Val Arg Arg Ile Phe Ser	
91	355 360 365	
92	ctt ata gga atg att gga cct gca gta ttc ctg gta gct gct ggc ttc	1209
93	Leu Ile Gly Met Ile Gly Pro Ala Val Phe Leu Val Ala Ala Gly Phe	

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95 att ggc tgt gat tat tct ttg gcc gtt gct ttc cta act ata tca aca 1257
96 Ile Gly Cys Asp Tyr Ser Leu Ala Val Ala Phe Leu Thr Ile Ser Thr
97 385          390          395          400
98 aca ctg gga ggc ttt tgc tct tct gga ttt agc atc aac cat ctg gat 1305
99 Thr Leu Gly Gly Phe Cys Ser Ser Gly Phe Ser Ile Asn His Leu Asp
100          405          410          415
101 att gct cct tcg tat gct ggt atc ctc ctg ggc atc aca aat aca ttt 1353
102 Ile Ala Pro Ser Tyr Ala Gly Ile Leu Leu Gly Ile Thr Asn Thr Phe
103          420          425          430
104 gcc act att cca gga atg gtt ggg ccc gtc att gct aaa agt ctg acc 1401
105 Ala Thr Ile Pro Gly Met Val Gly Pro Val Ile Ala Lys Ser Leu Thr
106          435          440          445
107 cct gat aac act gtt gga gaa tgg caa acc gtg ttc tat att gct gct 1449
108 Pro Asp Asn Thr Val Gly Glu Trp Gln Thr Val Phe Tyr Ile Ala Ala
109          450          455          460
110 gct att aat gtt ttt ggt gcc att ttc ttt aca cta ttc gcc aaa ggt 1497
111 Ala Ile Asn Val Phe Gly Ala Ile Phe Phe Thr Leu Phe Ala Lys Gly
112          465          470          475          480
113 gaa gta caa aac tgg gct ctc aat gat cac cat gga cac aga cac 1542
114 Glu Val Gln Asn Trp Ala Leu Asn Asp His His Gly His Arg His
115          485          490          495
116 tgaaggaacc aataaataat cctgcctcta ttaatgtatt tttattttatc atgtaacctc 1602
117 aaagtgcctt ctgtattgtg taagcattct atgtcttttt ttaattgtac ttgtattaga 1662
118 tttttaaggc ctataatcat gaaatatacac tagttgccag aataataaaa tgaactgtgt 1722
119 ttaattatga ataatatgta agctaggact tctacttttag gttcacatac ctgcctgcta 1782
120 gtccgggaac atgaagtagg acagttctgt tgatttttta gggccatact aaaggggaatg 1842
121 agctgaaaca gacctcctga tacctttgct taattaaact agatgataat tctcaggtac 1902
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129 atgcctgtaa tcccagcact ttgggggggt gaggtgggag aatcatgaga tcaggagttc 2382
130 gagaccagcc tggccagcat ggtgaaaccc catctctact aaaaatacaa aaaattagct 2442
131 gggcgtgggt acggggcgct gtaatcccag atactcagga ggctgaggtg ggagaatcac 2502
132 ttgaacctgg gaggtggaag ttgcagtga ccaagatcac gccactgcac tccagcctgg 2562
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142 Thr Asp Arg Thr Pro Leu Leu Pro Gly Ala Pro Arg Ala Glu Ala Ala
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149           65                70                75                80
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151           85                90                95
152   Thr Gly Lys Lys Tyr Gln Trp Asp Ala Glu Thr Gln Gly Trp Ile Leu
153           100               105               110
154   Gly Ser Phe Phe Tyr Gly Tyr Ile Ile Thr Gln Ile Pro Gly Gly Tyr
155           115               120               125
156   Val Ala Ser Lys Ile Gly Gly Lys Met Leu Leu Gly Phe Gly Ile Leu
157           130               135               140
158   Gly Thr Ala Val Leu Thr Leu Phe Thr Pro Ile Ala Ala Asp Leu Gly
159           145               150               155               160
160   Val Gly Pro Leu Ile Val Leu Arg Ala Leu Glu Gly Leu Gly Glu Gly
161           165               170               175
162   Val Thr Phe Pro Ala Met His Ala Met Trp Ser Ser Trp Ala Pro Pro
163           180               185               190
164   Leu Glu Arg Ser Lys Leu Leu Ser Ile Ser Tyr Ala Gly Ala Gln Leu
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166   Gly Thr Val Ile Ser Leu Pro Leu Ser Gly Ile Ile Cys Tyr Tyr Met
167           210               215               220
168   Asn Trp Thr Tyr Val Phe Tyr Phe Phe Gly Thr Ile Gly Ile Phe Trp
169           225               230               235               240
170   Phe Leu Leu Trp Ile Trp Leu Val Ser Asp Thr Pro Gln Lys His Lys
171           245               250               255
172   Arg Ile Ser His Tyr Glu Lys Glu Tyr Ile Leu Ser Ser Leu Arg Asn
173           260               265               270
174   Gln Leu Ser Ser Gln Lys Ser Val Pro Trp Val Pro Ile Leu Lys Ser
175           275               280               285
176   Leu Pro Leu Trp Ala Ile Val Val Ala His Phe Ser Tyr Asn Trp Thr
177           290               295               300
178   Phe Tyr Thr Leu Leu Thr Leu Leu Pro Thr Tyr Met Lys Glu Ile Leu
179           305               310               315               320
180   Arg Phe Asn Val Gln Glu Asn Gly Phe Leu Ser Ser Leu Pro Tyr Leu
181           325               330               335
182   Gly Ser Trp Leu Cys Met Ile Leu Ser Gly Gln Ala Ala Asp Asn Leu
183           340               345               350
184   Arg Ala Lys Trp Asn Phe Ser Thr Leu Cys Val Arg Arg Ile Phe Ser
185           355               360               365
186   Leu Ile Gly Met Ile Gly Pro Ala Val Phe Leu Val Ala Ala Gly Phe
187           370               375               380
188   Ile Gly Cys Asp Tyr Ser Leu Ala Val Ala Phe Leu Thr Ile Ser Thr
189           385               390               395               400
190   Thr Leu Gly Gly Phe Cys Ser Ser Gly Phe Ser Ile Asn His Leu Asp
191           405               410               415
192   Ile Ala Pro Ser Tyr Ala Gly Ile Leu Leu Gly Ile Thr Asn Thr Phe

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193          420          425          430
194    Ala Thr Ile Pro Gly Met Val Gly Pro Val Ile Ala Lys Ser Leu Thr
195          435          440          445
196    Pro Asp Asn Thr Val Gly Glu Trp Gln Thr Val Phe Tyr Ile Ala Ala
197          450          455          460
198    Ala Ile Asn Val Phe Gly Ala Ile Phe Phe Thr Leu Phe Ala Lys Gly
199          465          470          475          480
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213          Met Lys Ser Pro Val Ser Asp Leu Ala Pro
214          1          5          10
215    agc gac ggc gag gag ggc tcg gac cgc aca ccg ctc ctg cag cgc gcc 161
216    Ser Asp Gly Glu Glu Gly Ser Asp Arg Thr Pro Leu Leu Gln Arg Ala
217          15          20          25
218    ccg cgg gcg gaa ccc gct cca gta tgc tgc tct gct cgt tac aac cta 209
219    Pro Arg Ala Glu Pro Ala Pro Val Cys Cys Ser Ala Arg Tyr Asn Leu
220          30          35          40
221    gca ttt ttg tcc ttt ttt ggt ttc ttc gtt ctc tat tca tta cgg gtg 257
222    Ala Phe Leu Ser Phe Phe Gly Phe Phe Val Leu Tyr Ser Leu Arg Val
223          45          50          55
224    aat ctg agc gtt gca cta gtg gac atg gtg gat tca aac aca act gcc 305
225    Asn Leu Ser Val Ala Leu Val Asp Met Val Asp Ser Asn Thr Thr Ala
226          60          65          70
227    aaa gat aat aga acg tcc tac gag tgt gca gag cat tct gct ccc ata 353
228    Lys Asp Asn Arg Thr Ser Tyr Glu Cys Ala Glu His Ser Ala Pro Ile
229          75          80          85          90
230    aaa gtt ctt cac aac caa acg ggt aaa aag tac cgg tgg gat gca gaa 401
231    Lys Val Leu His Asn Gln Thr Gly Lys Lys Tyr Arg Trp Asp Ala Glu
232          95          100          105
233    act caa gga tgg att ctc gga tct ttt ttc tat ggc tac atc atc aca 449
234    Thr Gln Gly Trp Ile Leu Gly Ser Phe Phe Tyr Gly Tyr Ile Ile Thr
235          110          115          120
236    caa att cct gga gga tat gtt gcc agc aga agt ggg ggg aag ctg ttg 497
237    Gln Ile Pro Gly Gly Tyr Val Ala Ser Arg Ser Gly Gly Lys Leu Leu
238          125          130          135
239    cta gga ttc ggg atc ttt gct aca gct atc ttc acc ctg ttc act ccc 545
240    Leu Gly Phe Gly Ile Phe Ala Thr Ala Ile Phe Thr Leu Phe Thr Pro
241          140          145          150
242    ctc gct gca gat ttc gga gtc gga gcc ctt gtt gca ctc agg gca cta 593

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Use of <220> Feature(NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32)  
(Sec.1.823 of new Rules)

Seq#:10,12

## VARIABLE LOCATION SUMMARY

PATENT APPLICATION: US/10/823,506

DATE: 09/17/2004

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Input Set : N:\Crif3\RULE60\10823506.raw

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Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of &lt;220&gt; to &lt;223&gt; is MANDATORY if n's or Xaa's are present.

in &lt;220&gt; to &lt;223&gt; section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:5; N Pos. 13,16  
 Seq#:6; N Pos. 21  
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 Seq#:9; Xaa Pos. 95,99,102,113,114,116,123,132,133,136,137,138,141,144,145  
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 Seq#:9; Xaa Pos. 188,197,199,200,202,207,212,219,231,232,234,235,236,238  
 Seq#:9; Xaa Pos. 239,242,243,246,250,253,254,257,258,259,260,264,265,271  
 Seq#:9; Xaa Pos. 274,283,284,285,286,288,294,295,298,308,310,315,318,319  
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 Seq#:9; Xaa Pos. 474,482,486,487,488,491,495  
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## VARIABLE LOCATION SUMMARY

PATENT APPLICATION: US/10/823,506

DATE: 09/17/2004

TIME: 11:38:32

Input Set : N:\Crif3\RULE60\10823506.raw

Output Set: N:\CRF4\09172004\J823506.raw

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Seq#:11; Xaa Pos. 431,436,439,442,444,445,447,450,453,458,459,461,462,466  
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Seq#:12; Xaa Pos. 2,3,6,8,10,11,12,16,17,20,21,22,23,24,25,27,29,31,34,42  
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## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/823,506

DATE: 09/17/2004

TIME: 11:38:32

Input Set : N:\Crif3\RULE60\10823506.raw

Output Set : N:\CRF4\09172004\J823506.raw

L:10 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD  
L:405 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:5  
L:405 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:5  
L:405 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0  
L:414 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:6  
L:414 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:6  
L:414 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0  
L:635 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:48  
M:341 Repeated in SeqNo=9  
L:732 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:10, <213>  
ORGANISM:Artificial Sequence  
L:732 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:10, <213>  
ORGANISM:Artificial Sequence  
L:732 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10,Line#:732  
L:733 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:10  
L:733 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:10  
L:733 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0  
M:341 Repeated in SeqNo=10  
L:807 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0  
M:341 Repeated in SeqNo=11  
L:905 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:12, <213>  
ORGANISM:Artificial Sequence  
L:905 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:12, <213>  
ORGANISM:Artificial Sequence  
L:905 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:12,Line#:905  
L:906 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:12  
L:906 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:12  
L:906 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0  
M:341 Repeated in SeqNo=12